

Amendments to the Specification:

In the paragraph under the title "CROSS-REFERENCE TO RELATED APPLICATION" on page 1 please substitute the following paragraph:

--This application is a continuation of U.S. Patent Application No. 09/713,426, filed November 15, 2000, which is a continuation-in-part of U.S. Patent Application, Serial No. 09/430,409, filed October 29, 1999, which is an application claiming benefit under 35 USC 119(e) of a continuation of co-pending U.S. Provisional Application, Serial No. 60/121,453, filed February 24, 1999, the disclosures of which are hereby specifically incorporated by reference.--

Please substitute the second full paragraph on page 18 with the following amended version:

-- As shown in Table II I, 2.3% of the maize sequences (JM107MA2), 13.5% of the rice sequences and 27% of the *Arabidopsis* sequences showed significant similarity to protein coding sequences in GenBank. The estimated genome size of maize is about 2500 Mbp but as it is a segmental allotetraploid, the haploid maize genome size is 1250 Mbp, about ten times larger than *Arabidopsis* (See Arumuganathan, K. and E.D. Earle (1991) Plant Mol. Biol. Rep. 9:208; Gaut, B.S., and J.F. Doebley (1997) Proc. Natl. Acad. Sci. U.S.A. 94:6809). In agreement with this estimate, the percentage of genes found in random *Arabidopsis* BAC ends is about ten times higher than in maize shotgun reads.--

Please substitute the first full paragraph on page 19 with the following amended version:

-- The three genetically filtered libraries had fewer clones containing repetitive DNA than the unfiltered library. For example, 48.7% of the clones propagated in the unfiltered strain matched retro-transposons and other annotated repeats (Table II I).

In contrast, only 3.3% of the clones propagated in JM107 matched annotated repeats, and less than 10% matched all repetitive sequences. As predicted, the proportion of database matches to known coding sequences was increased four fold in the filtered versus the non-filtered libraries, with some differences between the different strains (Table II f). See also Figures 4-9. This increased the density of exons detected among maize filtered genomic sequences (i.e. 10%) to nearly that observed in rice (i.e. 13.5%). Given that introns comprise 60% of maize genes, and would not be recognized by protein database searches, it is likely that the actual number of recognizable genes represented in this collection is even higher, approaching 25%. As the number of proteins in public databases increases, the number of recognizable genes will also increase.--